

SEQUENCE LISTING

<110> Lowe, Keith S.  
 Gordon-Kamm, William J.  
 Klein, Theodore M.  
 Rasco-Gaunt, Sonriza  
 Cahoon, Rebecca E.  
 Sun, Xifan  
 Hoerster, George J.  
 Gregory, Carolyn A.  
 Nadimpalli, Ramgopal

<120> Transcriptional Activator Nucleic Acids,  
 Polypeptides, and Methods of Use Thereof

<130> 0943

<150> 60/107,643  
 <151> 1998-11-09

<160> 23

<170> FastSEQ for Windows Version 3.0

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 <212> DNA  
 <213> Zea mays

<220>  
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 <222> (69) ... (902)

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Met	Asp	Ser	Ser	Ser	Phe	Leu	Pro	Ala	Ala	Gly	Ala	Glu	Asn
1	5	10											

ggc	tcg	gcf	gcf	ggc	gcc	aac	aat	ggc	ggc	gct	gct	cag	cag	cat	158
Gly	Ser	Ala	Ala	Gly	Gly	Ala	Asn	Asn	Gly	Gly	Ala	Ala	Gln	Gln	His
15	20	25	30												

gcf	gcf	ccg	atc	cgf	gag	cag	gac	cgf	ctg	atc	cgf	aac	206		
Ala	Ala	Pro	Ala	Ile	Arg	Glu	Gln	Asp	Arg	Leu	Met	Pro	Ile	Ala	Asn
35	40	45													

gtg	atc	cgf	atc	atg	cgf	cgf	gtg	ctg	ccg	gcf	atc	gcf	aag	atc	tcg	254
Val	Ile	Arg	Ile	Met	Arg	Arg	Val	Leu	Pro	Ala	His	Ala	Lys	Ile	Ser	
50	55	60														

gac	gac	gcc	aag	gag	acg	atc	cag	gag	tgc	gtg	tcg	gag	tac	atc	agc	302
Asp	Asp	Ala	Lys	Glu	Thr	Ile	Gln	Glu	Cys	Val	Ser	Glu	Tyr	Ile	Ser	
65	70	75														

ttc	atc	acg	ggg	gag	gcc	aac	gag	cgf	tgc	cag	cgf	gag	cag	cgf	aag	350
Phe	Ile	Thr	Gly	Glu	Ala	Asn	Glu	Arg	Cys	Gln	Arg	Glu	Gln	Arg	Lys	
80	85	90														

acc	atc	acc	gcc	gag	gac	gtg	ctg	tgg	gcc	atg	agc	cgc	ctc	ggc	ttc	398
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Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe				
95	100	105	110	
gac gac tac gtc gag ccg ctc ggc gcc tac ctc cac cgc tac cgc gag				446
Asp Asp Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu				
115	120	125		
ttc gag ggc gac gcg cgc ggc gtc ggg ctc gtc ccg ggg gcc gcc cca				494
Phe Glu Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro				
130	135	140		
tcg cgc ggc ggc gac cac cac ccg cac tcc atg tcg cca gcg gcg atg				542
Ser Arg Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met				
145	150	155		
ctc aag tcc cgc ggg cca gtc tcc gga gcc gcc atg cta ccg cac cac				590
Leu Lys Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His				
160	165	170		
cac cac cac gac atg cag atg cac gcc gcc atg tac ggg gga acg				638
His His His Asp Met Gln Met His Ala Ala Met Tyr Gly Thr				
175	180	185	190	
gcc gtg ccc ccg ccg gcc ggg cct cct cac cac ggc ggg ttc ctc atg				686
Ala Val Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met				
195	200	205		
cca cac cca cag ggt agt agc cac tac ctg cct tac gcg tac gag ccc				734
Pro His Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro				
210	215	220		
acg tac ggc ggt gag cac gcc atg gct gca tac tat gga ggc gcc gcg				782
Thr Tyr Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Ala Ala				
225	230	235		
tac gcg ccc ggc aac ggc ggg agc ggc gac ggc agt ggc agt ggc ggc				830
Tyr Ala Pro Gly Asn Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly				
240	245	250		
ggc ggg agc gcg tcg cac aca ccg cag ggc agc ggc ggc ttg gag				878
Gly Gly Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu				
255	260	265	270	
cac ccg cac ccg ttc gcg tac aag tagctagttc gtacgtcggtt cgacttgagc				932
His Pro His Pro Phe Ala Tyr Lys				
275				
aagccatcga tctgctgatc tgaacgtacg ctgtattgtt cacgcacgtacg cgtacgtatc				992
ggccggcttagc tctcctgttt aagttgtact gtgattctgt cccggccggc tagcaactta				
gtatcttcct tcagtctcta gtttcttagc agtcgttagaa gtgttcaatg cttgccagtg	1052			
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a	1172			
	1173			

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 <213> Zea mays

<400> 2

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35 35	40 45	
Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp		
50 50	55 60	
Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile		
65 65	70 75	80
Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile		
85 85	90 95	
Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp		
100 100	105 110	
Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu		
115 115	120 125	
Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg		
130 130	135 140	
Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys		
145 145	150 155	160
Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His		
165 165	170 175	
His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val		
180 180	185 190	
Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His		
195 195	200 205	
Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr		
210 210	215 220	
Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala Tyr Ala		
225 225	230 235	240
Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly		
245 245	250 255	
Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro		
260 260	265 270	
His Pro Phe Ala Tyr Lys		
275		

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<220>  
 <223> primer

<400> 3

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20

<210> 4  
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 <212> DNA  
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<220>  
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<400> 4

gccggggacag aatcacagta

20

<210> 5  
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<220>

<223> primer  
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 tagtagcgag agccaatgga 20

<210> 6  
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<400> 6  
 cccggcccta aaacaacaca 20

<210> 7  
 <211> 481  
 <212> DNA  
 <213> Argemone mexicana

<220>  
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 <222> (44) ... (481)

<221> misc\_feature  
 <222> (1) ... (481)  
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 Met Glu Arg Gly  
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ggt ggt ggt ggt agt ggt ggt ttc cat gga tat cag aaa ctc 103  
 Gly Gly Gly Gly Ser Gly Gly Phe His Gly Tyr Gln Lys Leu  
 5 10 15 20

cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac 151  
 Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn  
 25 30 35

aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat 199  
 Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp  
 40 45 50

cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt 247  
 Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu  
 55 60 65

cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa 295  
 Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu  
 70 75 80

tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt 343  
 Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg  
 85 90 95 100

tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg 391  
 Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp  
 105 110 115

gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt 439  
 Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu  
 120 125 130  
  
 tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca 481  
 Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser  
 135 140 145  
  
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 <211> 146  
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 <213> Argemone mexicana  
  
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 20 25 30  
 Leu Ser Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val  
 35 40 45  
 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met  
 50 55 60  
 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu  
 65 70 75 80  
 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu  
 85 90 95  
 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu  
 100 105 110  
 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu  
 115 120 125  
 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg  
 130 135 140  
 Trp Ser  
 145  
  
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 Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met  
 1 5 10 15  
  
 gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc acc gct  
 Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala 95  
 20 25 30  
  
 ggg ttg aag ctg tca gtg tca gac atg aac atg agg cag cag gta gca 143  
 Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala  
 35 40 45

tca tca gat cac agt gca gcc aca gga gag gag aac gaa tgc acg gtg	191
Ser Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val	
50 55 60	
agg gag caa gac agg ttc atg cca atc gcc aac gtg att agg atc atg	239
Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met	
65 70 75	
cgc aag att ctc cct cca cac gca aaa atc tcg gac gat gca aaa gaa	287
Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu	
80 85 90 95	
aca atc caa gag tgc gtg tct gag tac atc agc ttc atc aca ggt gag	335
Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu	
100 105 110	
gcg aac gag cgt tgc cag agg gag cag cgg aag acc ata acc gca gag	383
Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu	
115 120 125	
gac gtg ctt tgg gcc atg agc aag ctt gga ttc gac gac tac atc gaa	431
Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu	
130 135 140	
ccg ttg acc atg tac ctt cac cgc tac cgt gaa ctt gag ggt gac cgc	479
Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg	
145 150 155	
acc tct atg agg ggt gaa cca ctc ggg aag agg act gtg gaa tac gcc	527
Thr Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala	
160 165 170 175	
acg ctt ggt gtt gct act gct ttt gtc cct cca ccc tat cat cac cac	575
Thr Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His	
180 185 190	
aat ggg tac ttt ggt gct gcc atg ccc atg ggg act tac gtt agg gaa	623
Asn Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu	
195 200 205	
gcg cca cca aat aca gcc tcc tcc cat cac cac cac cac cac cac	671
Ala Pro Pro Asn Thr Ala Ser Ser His His His His His His His His	
210 215 220	
cac cat gct cgt gga atc tcc aat gct cat gaa cca aat gct cgc tcc	719
His His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser	
225 230 235	
ata taaaattata taattatgac taggattcag aacaagactt gatgatgatt	772
Ile	
240	
agcttaactc tcagtaattg gtgctagagt actactgttg ttgaggatac ttatattat	832
aattaaggc tggaaaggga gtttagtatat tcctaattcct aactatgtgc atcttaatt	892
tatgaaatca ctttggatg aaaaaaaaaa aaaaaaaaaa	942

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 <211> 240  
 <212> PRT  
 <213> Glycine max

<400> 10

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Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala Gly  
20 25 30  
Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala Ser  
35 40 45  
Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val Arg  
50 55 60  
Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg  
65 70 75 80  
Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr  
85 90 95  
Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala  
100 105 110  
Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp  
115 120 125  
Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro  
130 135 140  
Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr  
145 150 155 160  
Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr  
165 170 175  
Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His Asn  
180 185 190  
Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu Ala  
195 200 205  
Pro Pro Asn Thr Ala Ser Ser His His His His His His His His His  
210 215 220  
His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile  
225 230 235 240

<210> 11

<211> 905

<212> DNA

<213> Veronia mespilifolia

<220>

<221> CDS

<222> (58) ... (699)

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Glu Arg Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His Pro  
5 10 15

aca tct gga atc caa caa tcg gat atg aag cta aag cta cca gaa atg 156  
Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu Met  
20 25 30

acc aac aat aac tcg tcc act gat gac aat gag tgc acc gtt cga gaa 204  
Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg Glu  
35 40 45

cag gac cgc ttc atg ccg ata gca aac gtg atc cgc atc atg cgg aag 252  
Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys  
50 55 60 65

atc ctt cct cca cat gcc aag atc tct gat gat gcc aaa gag acg atc Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile 70 75 80	300
caa gaa tgt gtt tca gag tac att agc ttt gtc aca ggc gag gca aat Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn 85 90 95	348
gac cgc tgc cag cgt gag caa agg aag acc atc aca gct gaa gat gtg Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val 100 105 110	396
ctc tgg gct atg agc aaa ctg gga ttt gat gat tat atc gag ccc ttg Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu 115 120 125	444
act gtg tat ctc cat cgc tac agg gag ttt gat ggt ggc gaa cgt gga Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg Gly 130 135 140 145	492
tcc ata agg ggt gag ccc ctt gtg aag agg agt act tct gat cct ggt Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro Gly 150 155 160	540
cac ttt ggg atg gct tct ttt gtg cct gct ttt cat atg ggt cat cat His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His His 165 170 175	588
aac ggc ttc ttt ggt cct gca agc att ggt ggt ttc ctg aaa gac cca Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp Pro 180 185 190	636
tcg agt gct ggc cct tcg gga cct gca gtc gct ggg ttt gag ccg tat Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro Tyr 195 200 205	684
gct cag tgt aaa gag taactgcaaa aagttaggggt tgggatgaga tgatgatgat Ala Gln Cys Lys Glu 210	739
ggtgtggtg gtggtggttt gttttgtttt gttctttctt tttttttct tctttcttt cttggtcatt gaggaacaaa cttacattgg ttcaacttgg ctaggcatgt aaacggtaa catgcttatac aagttagtagt ttcgatcaa aaaaaaaaaa aaaaaa	799 859 905
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Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp  
 100 105 110  
 Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro  
 115 120 125  
 Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg  
 130 135 140  
 Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro  
 145 150 155 160  
 Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His  
 165 170 175  
 His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp  
 180 185 190  
 Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro  
 195 200 205  
 Tyr Ala Gln Cys Lys Glu  
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<210> 13  
 <211> 763  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (1) ... (480)

<400> 13

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1 5 10 15	

cgc ctc ggc ttc gac gac tac gtc gcg ccc ctc ggc gcc ttc ctc cag	96
Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln	
20 25 30	

cgc atg cgc gac gac agc gac cac ggc ggt gaa gag cgc ggc ggc cct	144
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro	
35 40 45	

gca ggg cgt ggt ggc tcg cgc cgc ggc tcg tcg tcc ttg ccg ctc cac	192
Ala Gly Arg Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His	
50 55 60	

tgc ccg cag cag atg cac cac ctg cac cca gcc gtc tgc cgg cgt ccg	240
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro	
65 70 75 80	

cac cag agc gtg tcg cct gct gca gga tac gcc gtc cgg ccc gtt ccc	288
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro	
85 90 95	

cgc ccg atg cca gcc cgt ggg tac cgc atg cag ggc gga gac cac cgc	336
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg	
100 105 110	

agc gtg ggc ggc gtg gct ccc tgc agc tac gga ggg gcg ctc gtc cag	384
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln	
115 120 125	

gcc ggt gga acc caa cac gtt gta gga ttc cac gac gac gag gca agc	432
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser	
130 135 140	

tct tcg agt gaa aat ccg ccg gag ggg cgt gcc gct ggc tcg aac 480  
Ser Ser Ser Glu Asn Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn  
145 150 155 160

tagcctagct tctcagttcc ccgtgtacaa taagaggggc ggtcgccgcg ccgcgcgcg 540  
cccttgggtt gggccggcgt ctagctgca gtttggttt taaactaacg agccttaggt 600  
agctgggtca cgcgcgcac ctcgcccac gtcgcccgtcg tcgtcggcat ggacttaacc 660  
ggcggggccct gtttattt ctcaagttt tagccaacgc actgttcggt gcgttccata 720  
attnaattna ccatgttgcct ctcgaaaaaa aaaaaaaaaaaa aaa 763

<210> 14  
<211> 160  
<212> PRT  
<213> Zea mays

<400> 14  
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Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln 20 25 30  
Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro 35 40 45  
Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His 50 55 60  
Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro 65 70 75 80  
His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro 85 90 95  
Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg 100 105 110  
Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln 115 120 125  
Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser 130 135 140  
Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn 145 150 155 160

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<212> DNA  
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<221> misc\_feature  
<222> (1)...(622)  
<223> n = A,T,C or G

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Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu  
1 5 10 15

cca ccg gag ctt ccc aaa gaa gca gtg gcg acc gac gaa gca ccg ccg 95  
Pro Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro  
20 25 30

cca atg ggc aac aac aac acg gaa tcg gcg acg gcg acg atg gtc 143  
Pro Met Gly Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val

35

40

45

cg <sup>g</sup> gag cag gac cg <sup>g</sup> ctg atg ccc gt <sup>g</sup> gcc aac gt <sup>g</sup> tcc cg <sup>c</sup> atc atg			191
Arg Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met			
50	55	60	
cg <sup>c</sup> caa gt <sup>g</sup> ctg cct cg <sup>g</sup> tac gc <sup>c</sup> aag atc tcc gac gac gc <sup>c</sup> can gaa			239
Arg Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu			
65	70	75	
gt <sup>n</sup> atc caa gaa ttg ctn ttc gga att tca tca ctt nc <sup>g</sup> tcc tgg cg <sup>a</sup>			287
Xaa Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg			
80	85	90	95
gg <sup>c</sup> gaa acg aag cg <sup>g</sup> tgc cac acc gag cg <sup>c</sup> cg <sup>c</sup> aag acc gtc acc tcc			335
Gly Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser			
100	105	110	
gaa gac atc gt <sup>g</sup> tgg gc <sup>c</sup> atg agc cg <sup>c</sup> ctc gg <sup>c</sup> ttc gac gac tac gtc			383
Glu Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val			
115	120	125	
cg <sup>c</sup> ccc ctc gg <sup>c</sup> gc <sup>c</sup> ttc ctc cag cg <sup>c</sup> atg cg <sup>c</sup> gac nac agc gaa cac			431
Ala Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His			
130	135	140	
gg <sup>g</sup> ggt gaa aac gc <sup>g</sup> gc <sup>g</sup> gc <sup>c</sup> tgc ang gg <sup>g</sup> tng tgg tcn cg <sup>c</sup> cg <sup>c</sup> ggg			479
Gly Gly Asn Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly			
145	150	155	
tc <sup>g</sup> tct nct tgg cg <sup>c</sup> tcc ctt gc <sup>c</sup> gca ana gat gac aac ttg cac caa			527
Ser Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln			
160	165	170	175
ac <sup>g</sup> tct gc <sup>c</sup> ggg ntc gga cca aaa ctn ttc cct gtt gca gga ata ccc			575
Thr Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro			
180	185	190	
gt <sup>c</sup> cng gg <sup>c</sup> cnt tcc ccc ccn aat cca acc att tgg ttt ccc ctt gc			622
Val Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu			
195	200	205	

<210> 16  
 <211> 206  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> VARIANT  
 <222> (1)...(206)  
 <223> Xaa = Any Amino Acid

<400> 16  
 Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu Pro  
 1 5 10 15  
 Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro Pro  
 20 25 30  
 Met Gly Asn Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val Arg  
 35 40 45  
 Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met Arg  
 50 55 60

Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Asp Ala Xaa Glu Xaa  
 65 70 75 80  
 Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg Gly  
 85 90 95  
 Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser Glu  
 100 105 110  
 Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Ala  
 115 120 125  
 Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His Gly  
 130 135 140  
 Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly Ser  
 145 150 155 160  
 Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln Thr  
 165 170 175  
 Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro Val  
 180 185 190  
 Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu  
 195 200 205

<210> 17  
 <211> 1121  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (3)...(1121)

<400> 17

gc acg agg gaa act gga ggc ttt cat ggc tac cgc aag ctc ccc aac	47
Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn	
1 5 10 15	
aca acc tct ggg ttg aag ctg tca gtg tca gac atg aac atg aac atg	95
Thr Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met	
20 25 30	
agg cag cag cag gta gca tca tca gat cag aac tgc agc aac cac agt	143
Arg Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser	
35 40 45	
gca gca gga gag gag aac gaa tgc acg gtg agg gag caa gac agg ttc	191
Ala Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe	
50 55 60	
atg cca atc gct aac gtg ata cgg atc atg cgc aag att ctc cct cca	239
Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro	
65 70 75	
cac gca aaa atc tcc gat gat gca aag gag aca atc caa gag tgc gtg	287
His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val	
80 85 90 95	
tcg gag tac atc agc ttc atc acc ggg gag gcc aac gag cgt tgc cag	335
Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln	
100 105 110	
agg gag cag cgc aag acc ata acc gca gag gac gtg ctt tgg gca atg	383
Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met	
115 120 125	
agt aag ctt gga ttc gac gac tac atc gaa ccg tta acc atg tac ctt	431

Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu		
130	135	140
cac cgc tac cgt gag ctg gag ggt gac cgc acc tct atg agg ggt gaa		479
His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu		
145	150	155
ccg ctc ggg aag agg act gtg gaa tat gcc acg ctt gct act gct ttt		527
Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe		
160	165	170
175		
gtg ccg cca ccc ttt cat cac cac aat ggc tac ttt ggt gct gcc atg		575
Val Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met		
180	185	190
ccc atg ggg act tac gtt agg gaa acg cca cca aat gct gcg tca tct		623
Pro Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser		
195	200	205
cat cac cat gga atc tcc aat gct cat gaa cca aat gct cgc tcc		671
His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser		
210	215	220
ata taa aat taa tga aga gta ctg ttc agt agg aga aca aga ctt ctt		719
Ile * Asn * * Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu		
225	230	235
gga ctt gat tag ctt aac tct cag tga ttg gtg tta gag tac tgt tgt		767
Gly Leu Asp * Leu Asn Ser Gln * Leu Val Leu Glu Tyr Cys Cys		
240	245	250
tga gga tgg tta att tta taa tta agg gct ggg aat tgg gga gtt agt		815
* Gly Trp Leu Ile Leu * Leu Arg Ala Gly Asn Trp Gly Val Ser		
255	260	
ata tat tcc taa tcc taa tta tgt gca tct tta att tat gga ata act		863
Ile Tyr Ser * Ser * Leu Cys Ala Ser Leu Ile Tyr Gly Ile Thr		
265	270	275
ttg ttt ttt gtt tta act tct gat aat ttg gat ttt ctg atg ttt aat		911
Leu Phe Phe Val Leu Thr Ser Asp Asn Leu Asp Phe Leu Met Phe Asn		
280	285	290
gtg gtt ttg tct atc cct tat taa cag tgc caa gct taa ggt ttt agc		959
Val Val Leu Ser Ile Pro Tyr * Gln Cys Gln Ala * Gly Phe Ser		
295	300	305
cat gct cca aaa tgg aat act tgt act gtt atg ttg ttc tgg tag tga		1007
His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu Phe Trp * *		
310	315	320
tgg tga tga aac ctg caa gtt atg ttt atg tat aaa gcc act att gat		1055
Trp * * Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp		
325	330	335
caa aat tag aga aat tat cat tta ata agt atc ctc cca tgt taa ttt		1103
Gln Asn * Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys * Phe		
340	345	350
taa aaa aaa aaa aaa aaa		1121
* Lys Lys Lys Lys Lys		
355		

<210> 18  
<211> 355  
<212> PRT  
<213> Glycine max

<400> 18

Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr  
1 5 10 15  
Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met Arg  
20 25 30  
Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser Ala  
35 40 45  
Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met  
50 55 60  
Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His  
65 70 75 80  
Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser  
85 90 95  
Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg  
100 105 110  
Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser  
115 120 125  
Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu His  
130 135 140  
Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Pro  
145 150 155 160  
Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe Val  
165 170 175  
Pro Pro Pro Phe His His Asn Gly Tyr Phe Gly Ala Ala Met Pro  
180 185 190  
Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser His  
195 200 205  
His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile  
210 215 220  
Asn Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu Gly Leu Asp Leu  
225 230 235 240  
Asn Ser Gln Leu Val Leu Glu Tyr Cys Cys Gly Trp Leu Ile Leu Leu  
245 250 255  
Arg Ala Gly Asn Trp Gly Val Ser Ile Tyr Ser Ser Leu Cys Ala Ser  
260 265 270  
Leu Ile Tyr Gly Ile Thr Leu Phe Phe Val Leu Thr Ser Asp Asn Leu  
275 280 285  
Asp Phe Leu Met Phe Asn Val Val Leu Ser Ile Pro Tyr Gln Cys Gln  
290 295 300  
Ala Gly Phe Ser His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu  
305 310 315 320  
Phe Trp Trp Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp  
325 330 335  
Gln Asn Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys Phe Lys Lys  
340 345 350  
Lys Lys Lys  
355

<210> 19  
<211> 796  
<212> DNA  
<213> Glycine max

<220>  
<221> CDS

<222> (1) ... (513)

<400> 19  
gca cga gca atg gcg gga gtg agg gaa cag gac cag tac atg ccg ata 48  
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile  
1 5 10 15

gcg aac gtg ata agg atc atg cgt cgg att ctg cca gcg cac gcg aag 96  
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys  
20 25 30

atc tca gac gac gcg aag gag acg atc cag gag tgc gtg tct gag tac 144  
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr  
35 40 45

atc agt ttc atc acg gcg gag gcg aac gag cgg tgc cag cgg gag cag 192  
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln  
50 55 60

cgg aag acg gtg acc gca gag gat gtg ttg tgg gcg atg gag aag ctt 240  
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu  
65 70 75 80

ggc ttt gac aac tac gct cac cct ctc tct ctt tac ctt cac cgc tac 288  
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr  
85 90 95

cgc gag agt gaa gga gaa cct gct tct gtc aga cgc gct tct tct gca 336  
Arg Glu Ser Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala  
100 105 110

atg ggg atc aat aat atg gtg cac cca cct tat att aat tct cat 384  
Met Gly Ile Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His  
115 120 125

ggc ttt gga atg ttt gat ttt gac cca tca tcg caa ggg ttt tac agg 432  
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg  
130 135 140

gac gat cat aac gct gct tct gga tct ggt ttt gtt gcg cct ttt 480  
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Phe Val Ala Pro Phe  
145 150 155 160

gat cct tat gct aac atc aaa cgt gat gcc ctg tgatcatgta agaacaacaa 533  
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu  
165 170

ctagtgcatg ctgcgttttc acttggttag ttatattcaa gcacaagcac atgcagggtgc 593  
agctgcact attagcttc atctacaaat ctgttttcct ctcttcttct catgctttaa 653  
ttatatttagag acaatacttg ttattcattg ttatgctcaa ttgctagctt ctattcatcg 713  
tcgactgtct gtattgttga tgttcattac agtaacagat aagatggtaa ctgctttact 773  
acttcaaaaa aaaaaaaaaaaa aaa 796

<210> 20  
<211> 171  
<212> PRT  
<213> Glycine max

<400> 20  
Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile  
1 5 10 15  
Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys

20	25	30
Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr		
35	40	45
Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln		
50	55	60
Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu		
65	70	80
Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr		
85	90	95
Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala		
100	105	110
Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His		
115	120	125
Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg		
130	135	140
Asp Asp His Asn Ala Ala Ser Gly Ser Gly Phe Val Ala Pro Phe		
145	150	155
Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu		
165	170	

<210> 21  
 <211> 1098  
 <212> DNA  
 <213> *Triticum aestivum*

<220>  
 <221> CDS  
 <222> (55) ... (894)

<400> 21

gcacgagcaa gtgcgagtc gactacctgc attgcacctt ggctagccct agac atg	57
Met	
1	

gag aac gac ggc gtc ccc aac gga cca gcg gcg ccg gca cct acc cag	105
Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr Gln	
5	10
15	

ggg acg ccg gtg gtg cgg gag cag gac cgg ctg atg ccg atc gcg aac	153
Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn	
20	25
30	

gtg atc cgc atc atg cgc cgt gcg ctc cct gcc cac gcc aag atc tcc	201
Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile Ser	
35	40
45	

gac gac gcc aag gag gcg att cag gaa tgc gtg tcc gag ttc atc agc	249
Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile Ser	
50	55
60	65

ttc gtc acc ggc gag gcc aac gaa cgg tgc cgc atg cag cac cgc aag	297
Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg Lys	
70	75
80	

acc gtc aac gcc gaa gac atc gtg tgg gcc cta aac cgc ctc ggc ttc	345
Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly Phe	
85	90
95	

gac gac tac gtc gtg ccc ctc agc gtc ttc ctg cac cgc atg cgc gac	393
Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg Asp	
100	105
110	

ccc gag gcg ggg aca ggt ggt gcc gct gca ggc gac agc cgc gcc gtc 441  
 Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala Val  
 115 120 125  
  
 acg agt gcg cct ccc cgc gcg gcc ccc gtc atc cac gcc gtc ccc 489  
 Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val Pro  
 130 135 140 145  
  
 ctg cag gct cag cgc ccg atg tac gcg ccc ccg gct ccg ttg cag gtt 537  
 Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln Val  
 150 155 160  
  
 gag aat cag atg cag cgg cct gtc tac gct ccc ccg gct ccg gtc cag 585  
 Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val Gln  
 165 170 175  
  
 gtt cag atg cag cgg ggc atc tat ggg ccc ccg gct cca gtc cac ggg 633  
 Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His Gly  
 180 185 190  
  
 tac gcc gtc gga atg gcg ccc gtc ccg gcc aac gtc ggc ggg cag tac 681  
 Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln Tyr  
 195 200 205  
  
 cag gtc ttc ggc gga gag ggt gtc atg gcc cag caa tac tac ggg tac 729  
 Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly Tyr  
 210 215 220 225  
  
 ggg tac gag gaa gga gcg tac ggc gca ggt agc agc aac gga gga gcc 777  
 Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly Ala  
 230 235 240  
  
 gcc att ggc gac gag gag agc tcg tcc aac ggc gtc ccg gca ccg ggg 825  
 Ala Ile Gly Asp Glu Glu Ser Ser Asn Gly Val Pro Ala Pro Gly  
 245 250 255  
  
 gag ggc atg ggg gag cca gag cca gag cca gca gaa gaa tcg cat 873  
 Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser His  
 260 265 270  
  
 gac aag ccc gtc caa tct ggc tagtcgcgtg cgccggcgcc gtttagcttct 924  
 Asp Lys Pro Val Gln Ser Gly  
 275 280  
  
 gcgtccctgtg tactgtata atttgccgtg tcgatccggc catggttgt gtgtgcgtag 984  
 tgcttatcta atgtgggctt gtcctctagt aattcatgta ttgcttatct aatgtggact  
 tgcctcttag taattcatgt actctttgct gttgaaaaaaaa aaaaaaaaaaaa aaaa  
 1044  
 1098  
  
 <210> 22  
 <211> 280  
 <212> PRT  
 <213> Triticum aestivum  
  
 <400> 22  
 Met Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr  
 1 5 10 15  
 Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala  
 20 25 30  
 Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile  
 35 40 45  
 Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile  
 50 55 60

Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg  
 65 70 75 80  
 Lys Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly  
 85 90 95  
 Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg  
 100 105 110  
 Asp Pro Glu Ala Gly Thr Gly Ala Ala Ala Gly Asp Ser Arg Ala  
 115 120 125  
 Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val  
 130 135 140  
 Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln  
 145 150 155 160  
 Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val  
 165 170 175  
 Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His  
 180 185 190  
 Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln  
 195 200 205  
 Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly  
 210 215 220  
 Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly  
 225 230 235 240  
 Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro  
 245 250 255  
 Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser  
 260 265 270  
 His Asp Lys Pro Val Gln Ser Gly  
 275 280

<210> 23

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> LEC1 consensus protein sequence

<221> VARIANT

<222> (1)...(65)

<223> Xaa = Any Amino Acid

<400> 23

Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met  
 1 5 10 15  
 Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu  
 20 25 30  
 Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu  
 35 40 45  
 Ala Asn Xaa Arg Cys Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu  
 50 55 60  
 Xaa  
 65